## REMARKS

The Office Action mailed September 16, 2004, has been received and reviewed. Claims 2 through 5 and 7 through 20 were pending. Claims 7 through 17 were withdrawn from consideration as drawn to the non-elected subject matter, leaving claims 2 through 5 and 18 through 20 under consideration. All claims under consideration were rejected in the Office Action. Claims 2 and 18 are amended and claims 5, 19 and 20 are canceled herein. Claims 1 and 6 were earlier canceled. All amendments and cancellations are made without prejudice or disclaimer. Applicants respectfully request reconsideration of the application in view of the amendments and remarks set forth herein.

**Amendments to Specification and Sequence Rules Compliance**

The Office Action states that the nucleotide sequences at page 2, paragraph [0004] of the specification are not identified by sequence identification numbers, and included a Notice to Comply. The specification has been amended to include the requested sequence identification numbers and a replacement Sequence Listing is submitted herewith as Exhibit A. Directions are provided to substitute the replacement Sequence Listing for the earlier one. No new matter has been added. A computer readable copy of the Sequence Listing and the required Statement also accompany this response.

**Claim Objections**

Claims 19 and 20 were objected to in the Office Action as allegedly drawn in the alternative to the subject matter of non-elected claims. Claims 19 and 20 have been canceled, rendering this objection moot. Claim 5 was objected to based on a typographical error. Claim 5 has been canceled, rendering this objection moot.

Claim 18 was rejected to because of an informality. Claim 18 has been amended as suggested in the Office Action to correct the placement of the comma. It is respectfully requested that the objection be withdrawn.

**35 U.S.C. § 112 Rejections**

Claim 5 was rejected in the Office Action under 35 U.S.C. § 112, first paragraph, as assertedly failing to comply with the enablement requirement. Claim 5 has been canceled herein, rendering this rejection moot.

Claims 2 through 5 and 18 through 20 were rejected in the Office Action under 35 U.S.C. § 112, second paragraph, as assertedly being indefinite for failing to particularly point out and distinctly claim the subject matter of the invention. Claims 5, 19 and 20 have been canceled, rendering this rejection moot as to these claims.

Claims 2 and 18 were asserted in the Office Action to be indefinite as they " do not recite an active process step that clearly relates back to the objective recited in the preamble of the claims," which is stated to be "'necessary to give life meaning and vitality' to the claims." (Office Action at page 8). The Office Action further states that the phrase "such as" would render the claims indefinite.

As amended, independent claim 2 and independent claim 18 now each include the elements of "performing a specificity test to identify said transcription factors, wherein said transcription factors bind to said first SEQ ID NO: 1 and to said second SEQ ID NO: 1." Additionally, the phrase "such as" has been removed from the preamble of the claims. Accordingly, it is submitted that amended claims 2 and 18, with the claims dependent therefrom are definite.

**35 U.S.C. § 102 Anticipation Rejections**

Claims 2 through 4 and 18 through 20 are rejected under 35 U.S.C. §102(b) as assertedly being anticipated by Sekido *et al.* Claims 19 and 20 are canceled herein, rendering this rejection moot to those claims.

A claim is anticipated only if each and every element as set forth in the claim is found, either expressly or inherently described, in a single prior art reference. *Verdegaal Brothers v. Union Oil Co. of California*, 2 USPQ2d 1051, 1053 (Fed. Cir. 1987). The identical invention must be shown in as complete detail as is contained in the claim. *Richardson v. Suzuki Motor Co.*, 9 USPQ2d 1913, 1920 (Fed. Cir. 1989). After carefully considering the cited prior art reference, Applicants submit that Sekido *et al.* fails to anticipate claims 2 through 4 and 18, as

each and every element set forth in the amended claims is not disclosed in the Sekido *et al.* reference.

Amended independent claim 2 includes the elements of "providing cells with a nucleic acid sequence comprising a first SEQ ID NO: 1 and a second SEQ ID NO: 1 separated by N as bait for identifying said transcription factors, **wherein N is a spacer sequence less than 400 base pairs long**" (emphasis added). Support for this amendment can be found in the specification, for example, at page 6 (paragraph 0013). Similarly, amended claim 18 includes the elements of "providing cells with a nucleic acid sequence comprising twice a CACCT sequence (SEQ ID NO: 1) as bait for the screening of a library encoding potential transcription factors, wherein the at least twice a CACCT sequence is a first SEQ ID NO: 1 and a second SEQ ID NO: 1 separated by N as bait, **wherein N is a spacer sequence less than 400 base pairs long**" (emphasis added). Support for this amendment can also be found in the specification at page 6 (paragraph 0013). Further, each of these amended independent claims includes the elements of "performing a specificity test to identify said transcription factors, wherein said transcription factors bind to said first SEQ ID NO: 1 and to said second SEQ ID NO: 1." Support for this amendment can be found at pages 39 and 40 of the specification (paragraph 0103). Accordingly, these claims define over the cited reference as containing elements not disclosed therein.

Additionally, Sekido *et al.* further fails to disclose "screening of a library encoding potential transcription factors," which is an element of claim 18.

As independent claims 2 and 18 include elements not disclosed in Sekido *et al.*, it is requested the rejection of these claims, with dependent claims 3 and 4, be withdrawn.

**35 U.S.C. § 103 (a) Obviousness Rejections**

Obviousness rejection based on Mak *et al.* in view of Sekido *et al.*

Claims 2 through 4 and 18 through 20 stand rejected under 35 U.S.C. 103(a) as assertedly being obvious over Mak *et al.* in view of Sekido *et al.* Claims 19 and 20 have been canceled making this rejection moot, as to them. With respect to the remaining claims, applicants respectfully submit that the amended claims define over the combination suggested by the Office Action.

On page 14, the Office Action states that Mak *et al.* teaches a process that can be used to screen a cDNA library to identify and isolate cDNA molecules encoding novel bHLH transcription factors comprising providing a cell comprising multiple copies of an E box, which is used as bait in the process. On the same page, the Office Action alleges that Sekido *et al.* teaches a promoter region comprising a polynucleotide sequence comprising multiple E-box sites having the sequence "CACCT" to which the δEF1 transcription factor, comprising separated clusters of zinc fingers, may bind and which may be used to identify the bound transcription factor. The Office Action then claims it would have been obvious to one of skill in the art to combine these references to identify transcription factors like basic helix-loop-helix (HLH) transcription factors, such as those disclosed by Mak *et al.*, and a zinc finger transcription factor like δEF1, as disclosed by Sekido *et al.*

As disclosed in Mak *et al.*, a functional bHLH DNA-binding motif consists of a dimerization of two HLH proteins which produces a *single* functional binding complex that interacts with a *single* DNA sequence, i.e. a *single* E-box. (Mak *et al.* page 1, column 1). As discussed in Sekido *et al.*, the δEF1 transcription factor has two zinc fingers that organize to form a *single* DNA binding domain that recognizes a *single* DNA binding site. (Sekido *et al.* page 778, column 2). As such, combining the references would produce a process that screens a cDNA library for transcription factors with *single* DNA-binding domains that bind to a *single* E-box site. Accordingly, were the references combined as suggested in the Office Action, the combination would not teach or suggest a process of screening a cDNA library for novel transcription factors wherein the transcription factors bind to a first DNA-binding site and **also** to a second DNA-binding site by means of separated zinc fingers - as found in amended claims 2 and 18. As such, the combination of the prior art references Mak *et al.* in view of Sekido *et al.* fails to teach or suggest all the claim limitations.

Moreover, no suggestion or motivation exists to combine the referenced teachings as suggested. Mak *et al.* explores the use of a yeast one-hybrid system to identify novel bHLH proteins, but neither suggests nor motivates one of skill in the art to use single E-box DNA-binding sites to screen for multiple zinc finger proteins that target more than a single DNA-binding site. (Mak *et al.* page 5, column 2). Sekido *et al.* discusses other binding proteins that use cooperating zinc finger motifs to form a single DNA binding domain with a single DNA binding

site, but fails to motivate or suggest identification of multiple zinc finger proteins that have multiple DNA binding domains and target multiple DNA binding sites.

Finally, the combined references teach the use of single E-box DNA bindings sites as bait for screening a cDNA library for novel transcription factors. The E-box site is a target of δEF1, and various bHLH transcription factors which recognize the single E-box domain with a single DNA binding domain. As such, a process for identifying transcription factors that recognize multiple binding domains separated by spacer sequences would not expect the E-box sequence, or an octamer of E-boxes, to be appropriate bait. One of skill in the art would expect an E-box domain as a bait to identify transcription factors similar to δEF1 and various bHLH transcription factors which recognize the single E-box domain with a single DNA binding domain. As such, one would not have had a reasonable expectation of success in using the combined teaching of the cited prior art references for the purpose of identifying transcription factors that target multiple DNA binding domains.

For the foregoing reasons, applicants respectfully request the obviousness rejection be withdrawn.

## CONCLUSION

Claims 2 through 4 and 18 are believed to be in condition for allowance, and an early notice thereof is respectfully solicited. Should the Office determine that the additional issues remain which might be resolved by a telephone conference, the Examiner is respectfully invited to contact the applicants' undersigned agent.

Respectfully submitted,

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